DELICAS - Association mapping and model phenotyping in sugarcane

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Rationales

The creation of new varieties, with high potential yield and resistant to pests, is a major objective to maintain the competitiveness of sugarcane sector in Reunion.

Inputs of genomics in sugarcane breeding have been limited to date, mainly by reason of the small number of identified molecular markers usable for breeding purpose.

In Reunion, sugarcane covers 27,000 hectares and generates more than 12,000 jobs. The whole sugarcane sector in Reunion produces 200,000 tons of sugar and 120,000 hectolitres of alcohol, 22% of the electricity of the island comes from the use of sugarcane residue .

Objectives and strategy

The DELICAS project aims at identifying molecular markers associated with genes implied in the elaboration of sugarcane yield or responsible for resistance to some pests, by using ecophysiological models, association mapping and by increasing the genome coverage with molecular markers. To achieve the objectives of the project, we will:
- elaborate methods and tools for model assisted phenotyping,
- phenotype of a core collection of 200 cultivars (i) for yield elaboration, supported by ecophysiological models and (ii) for resistance to the yellow leaf disease,
- genotype the core collection using several technologies (AFLP, DArT and SSR) to improve genome coverage and detect marker-trait association by association mapping.

Expected results

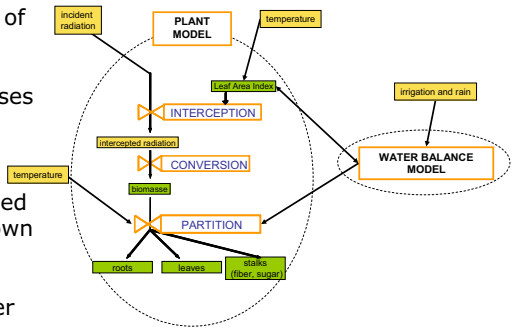
Expected results are (i) new methods and tools for model based phenotyping, (ii) a better knowledge of genetic determinism and the identification of chromosome areas involved in sugarcane yield elaboration or in resistance to the yellow leaf disease, and (iii) elaboration of tools for data management and exploitation.

Partnership

DELICAS is a public-private partnership between Cirad and eRcane, labelled by the Pôle de Compétitivité Qualitropic. eRcane is a breeding organism funded by the two sugar manufactures of Reunion: Sucrière de Reunion and Sucrerie de Bois-Rouge

Model assisted phenotyping

In a first step, we will assess the validity of the strategy of dissecting yield elaboration processes through model phenotyping. The performance of models will be tested on 20 cultivars grown in two contrasted environments in Reunion. The power of statistically optimized model parameters to (i) discriminate among genotypes and (ii) overcome G x E interactions will be compared with that of conventional phenotyping (direct trait observations).

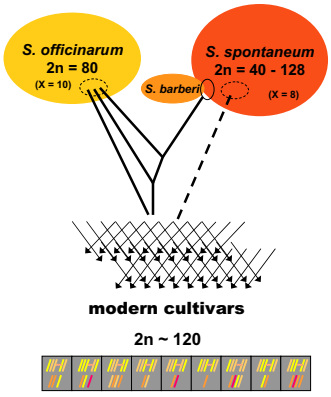


Phenotypic traits for production potential interact strongly with the environment, and represent the outcome of multiple processes difficult to measure and to tag at the genetic level. Plant growth modelling can describe yield formation dynamically as a set of interactive equations using only a small number of genotypic parameters. The different parameters participating in phenotype expression can be considered as synthetic component traits, presumably controlled by fewer genes than the complex agronomic traits and can be expected to be closer to gene or QTL. Two models of different nature will be used : EcoMeristem (plant level) and Mosicas (crop level).

In a second step, model assisted phenotyping of a 200 cultivar core collection will be carried out using data collected in two contrasted environments in Reunion.

Association mapping in sugarcane

Recent studies have detected significant linkage disequilibrium between markers up to 30 cM apart. Although extensive, LD drops sharply when markers are 5 cM or more apart. Many instances of linked markers cannot be recognized, largely due to the confounding effect of polyploidy. However, LD within a sample of cultivars appears as efficient as linkage analysis within a controlled progeny in terms of assigning markers to cosegregation groups.



The extent of LD in sugarcane is the consequence of the recent beginning of breeding of this crop. Only few generations separate modern cultivars from a limited number of founder sugarcane clones, limiting the number of meiosis and consequently the opportunity of chromosome recombination.

Funding